EXHIBIT 6

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Blast 2 Sequences results

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.15 [Oct-15-2006]

Matrix `BLOSUM62` gap open: `11` gap extension: `1`

x_dropoff: `50` expect: `10.0000` wordsize: `3` Filter ☐ View option `Standard`

Masking character option `X for protein, n for nucleotide` Masking color option `Black`

☐ Show CDS translation `Align`

Sequence 1: gi|6678678|ref|NP_032519.1|leptin [Mus musculus] >gi|730219|sp|P41160|LEP_MOUSE Leptin precursor (Obesity factor) >gi|603288|gb|AAA64564.1| ob >gi|726297|gb|AAA64213.1| obesity protein >gi|26326917|dbj|BAC27202.1| unnamed protein product [Mus musculus] >gi|74216350|dbj|BAE25117.1| unnamed protein product [Mus musculus] >gi|115545388|gb|AAI25246.1| Leptin [Mus musculus] >gi|1092655|prf||2024338A obeser gene Length = 167 (1 .. 167)

Sequence 2: gi|6981148|ref|NP_037208.1|leptin [Rattus norvegicus] >gi|1709436|sp|P50596|LEP_RAT Leptin precursor (Obesity factor) >gi|2144095|pir||I55622 rat ob - rat >gi|995615|dbj|BAA08529.1| leptin (ob product) [Rattus norvegicus] >gi|1018991|dbj|BAA08296.1| rat ob [Rattus sp.] >gi|9800646|gb|AAB34657.2| obese [Rattus norvegicus] Length = 167 (1 .. 167)
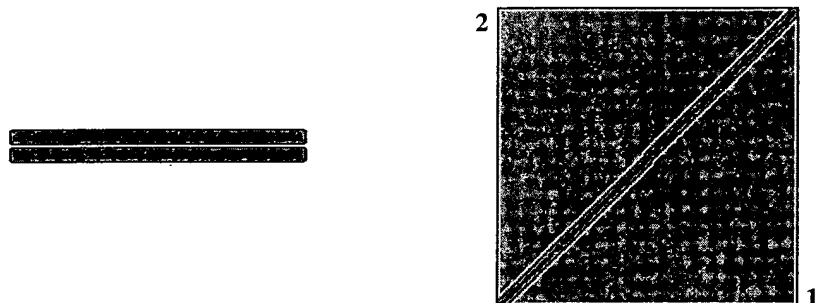
NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
Score = 322 bits (825),  Expect = 6e-87
Identities = 161/167 (96%), Positives = 165/167 (98%), Gaps = 0/167 (0%)

Query  1    MCWRPLCRFLWLWSYLSYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSAKQRVTGL  60
            MCWRPLCRFLWLWSYLSYVQAVPI KVQDDTKTLIKTIVTRINDISHTQSVSA+QRVTGL
Sbjct  1    MCWRPLCRFLWLWSYLSYVQAVPIHKVQDDTKTLIKTIVTRINDISHTQSVSARQRVTGL  60

Query  61   DFIPGLHPILSLSKMDQTLAVYQQVLTSLPSQNVLQIANDLENLRDLLHLLAFSKSCSLP  120
            DFIPGLHPILSLSKMDQTLAVYQQ+LTSLPSQNVLQIA+DLENLRDLLHLLAFSKSCSLP
Sbjct  61   DFIPGLHPILSLSKMDQTLAVYQQILTSLPSQNVLQIAHDLENLRDLLHLLAFSKSCSLP  120

Query  121  QTSGLQKPESLDGVLEASLYSTEVVALSRLQGSLQDILQQLDVSPEC  167
            QT GLQKPESLDGVLEASLYSTEVVALSRLQGSLQDILQQLD+SPEC
Sbjct  121  QTRGLQKPESLDGVLEASLYSTEVVALSRLQGSLQDILQQLDLSPEC  167
```

```
CPU time:        0.02 user secs.        0.01 sys. secs        0.03 total secs.

Lambda      K       H
  0.319    0.133    0.387

Gapped
Lambda      K       H
  0.267    0.0410    0.140


Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Sequences: 1
Number of Hits to DB: 324
Number of extensions: 121
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 167
Length of database: 1,565,033,500
Length adjustment: 124
Effective length of query: 43
Effective length of database: 1,565,033,376
Effective search space: 67296435168
Effective search space used: 67296435168
Neighboring words threshold: 9
X1: 16 ( 7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.8 bits)
S2: 73 (32.7 bits)
```